

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph starting on page 8, line 21 – page 9, line 7, with the following:

Figure 2: Structure and domains of the NFR5 protein. **a.** Schematic representation of the NFR5 protein domains. **b.** The amino acid sequence of NFR5 arranged in protein domains. Bold, conserved LysM residues. Bold and underlined residues conserved in protein kinase domains (KD); TM: transmembrane, SP: signal peptide. The asterisk indicates a stop codon in the *nfr5-3*; the black triangle a retrotransposon insertion in *nfr5-2* and the grey box defines the amino acids deleted in *nfr5-1*. **c.** Individual alignment of the three LysM motifs (M1, M2, M3) from NFR5, pea SYM10, *Medicago truncatula* (*M.t.*, Ac126779) rice (Ac103891), the single LysM in chitinase from *Volvox carteri* (Acc. No: T08150) and the pfam consensus. **d.** The divergent or absent activation loop (domain VIII) in the NFR5 family of receptor kinases is illustrated by alignment of kinase motifs VII, VIII and IX from *Arabidopsis* (At2g33580) NFR5, SYM10, *Medicago truncatula* (*M.t.*, Ac126779), rice (Ac103891) and the SMART consensus. Conserved domain VII aspartic acid is marked in bold and underlined. In Figures **2c** and **d**, the amino acids conserved in all aligned motifs are marked in black bold and amino acids conserved in two or more motifs are ~~marked in grey~~ underlined.

Please replace the paragraph starting on page 9, line 22 – page 10, line 8, with the following:

Figure 5. Positional cloning of the *NFR1* gene. **a.** Genetic map of the region surrounding the *NFR1* locus. Positions of the closest AFLP, microsatellite- and PCR-markers are given together with genetic distances in cM. **b.** Physical map of the *NFR1* locus. BAC clones 56L2, 16K18, 10M24, 36D15, 56K22 and TAC clones LjT05B16, LjT02D13, LjT211O02, which cover the region are shown. The numbers of recombination events detected with BAC and TAC end-markers or internal markers are given. Arrows indicate the positions of the

two markers (10M24-2, 56L2-2) delimiting the *NFR1* locus. UFD and HP correspond to the UFD1-like protein and the hypothetical protein encoded in the region. **c.** Exon-intron structure of the *NFR1* gene. Boxes correspond to exons, where LysM motifs are shown in ~~light grey~~ stippled boxes, trans-membrane region in black, kinase domains in ~~dark grey~~ hatched boxes. Dotted lines define introns and full lines define the 5' and 3' un-translated regions. The nucleotide length of all exons and introns are indicated. The numbers between brackets correspond to exon and intron 4, corresponding to alternative splicing.